GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2003, 17:21:34 ; Search time 256 Seconds
(without alignments)
3690.638 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 1799
Sequence: 1 MDLKALLSSLNDFASLSFAE.....LENKINIILSETDRDPLQVV 350

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1799	100.0	1053	22	AAH52212	Human AFP protein
2		1799	100.0	1574	22	AAH16397	Human cDNA sequenc
3		1799	100.0	1696	22	AAK60866	Human immune/haema
4		1799	100.0	1739	23	ABV23243	Human prostate exp
5		1799	100.0	1739	23	ABV29087	Human prostate exp
6		1793	99.7	1554	22	AAS44644	Human full-length
7		1763	98.0	1398	22	AAF59945	Human gene express
8		1725.5	95.9	1385	24	ABL60919	Human protein kina
9	c	1209.5	67.2	1686	23	AAS85172	DNA encoding novel
10		826.5	45.9	796	22	AAH07192	Human cDNA clone (
11		737	41.0	14969	22	AAK78763	Human immune/haema
12		644	35.8	462	22	AAL23953	Human breast cance
13		602	33.5	514	22	AAL15105	Human breast cance
14		578	32.1	1011	23	ABL07427	Drosophila melanog
15		578	32.1	2967	23	ABL10022	Drosophila melanog
16		578	32.1	3011	23	ABL07426	Drosophila melanog
17		538	29.9	513	22	AAS44816	Human contig polyn
18		467	26.0	394	25	ABX45683	Bovine EST associa
19	c	391	21.7	465	22	ABA46423	Human breast cell
20	c	391	21.7	465	22	ABA57019	Human foetal liver
21	c	391	21.7	465	22	AAK05073	Human brain expres
22	c	391	21.7	465	22	AAI15235	Probe #5168 for ge
23	c	391	21.7	465	22	AAI04973	Probe #4964 used t
24	c	391	21.7	465	23	ABS30297	Human liver single
25		386	21.5	249	21	AAC25260	Human secreted pro
26	c	370	20.6	208	22	ABA51524	Human breast cell
27	c	370	20.6	208	22	ABA69581	Human foetal liver
28	c	370	20.6	208	22	AAK17792	Human brain expres
29	c	370	20.6	208	22	AAI24414	Probe #14347 for g
30	c	370	20.6	208	22	AAI09950	Probe #9941 used t
31	c	370	20.6	208	23	ABS43283	Human liver single
32		362	20.1	495	23	AAS85169	DNA encoding novel
33		330	18.3	633	22	AAS34287	Human cDNA encodin
34		305	17.0	1104	24	ABN91378	Staphylococcus epi
35		305	17.0	3041	22	AAH55004	S. epidermidis gen
36		300	16.7	4159	20	AAX12944	Enterococcus faeca
37		300	16.7	4159	24	ABS98739	Enterococcus faeca
38		296	16.5	1083	22	AAH53378	S. epidermidis ope
39		291	16.2	522	23	AAS85171	DNA encoding novel
40		289.5	16.1	34088	23	AAS59566	Propionibacterium
41		288	16.0	3441	22	AAH54443	S. epidermidis gen
42		256	14.2	495269	24	ABQ67195	Listeria innocua c
43	c	256	14.2	3011208	24	ABQ69245	Listeria innocua D
44		249	13.8	1131	22	AAH53356	S. epidermidis ope
45	c	249	13.8	3014	22	AAH54966	S. epidermidis gen

ALIGNMENTS

RESULT 1
AAH52212
ID AAH52212 standard; cDNA; 1053 BP.
XX
AC AAH52212;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human AFP protein encoding cDNA sequence SEQ ID NO:239.
XX
KW Human; secreted protein; secretion; bacterial cell; fungal cell;
KW eukaryotic cell; fusion protein; maltose binding protein;
KW immunoglobulin constant region; polyhistidine tag; ss.
XX
OS Homo sapiens.
XX
PN WO200129221-A2.

```
XX
PD   26-APR-2001.
XX
PF   20-OCT-2000; 2000WO-US29052.
XX
PR   20-OCT-1999;   99US-0160712.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Conklin DC,  Yee DP;
XX
DR   WPI; 2001-300340/31.
DR   P-PSDB; AAG81361.
XX
PT   Isolated polypeptide for directing secretion of proteins of interest
PT   from a host cell including, e.g. bacteria, includes contiguous amino
PT   acid residues of polypeptide with specified amino acids -
XX
PS   Claim 9; Page 422-424; 617pp; English.
XX
CC   AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242
CC   to AAG81453. The secreted proteins can be used for directing the
CC   secretion of proteins of interest from a host cell including bacteria,
CC   fungal cells, and cultured higher eukaryotic cells. The present invention
CC   also describes fusion proteins, where a secreted protein of the invention
CC   is operably linked via a peptide bond or peptide linker to a second
CC   protein selected from the group consisting of maltose binding protein,
CC   an immunoglobulin constant region, a polyhistidine tag and a peptide
CC   given in AAG81453.
XX
SQ   Sequence 1053 BP; 279 A; 253 C; 247 G; 274 T; 0 other;

Alignment Scores:
Pred. No.:                2.56e-178       Length:          1053
Score:                    1799.00         Matches:         350
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       22              Gaps:            0

US-09-745-506-37 (1-350) x AAH52212 (1-1053)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
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Db          1 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 60

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 120

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 180

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 240

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 300

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
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Db        301 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 360

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 420

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
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Db        421 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 480

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
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Db        481 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 540

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
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Db        601 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 660

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
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Db        661 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 720

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
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Db        721 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 780

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerServalLeuGln 280
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Db        781 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 840

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
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Db        841 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 900

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
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Db        901 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 960

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
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Db        961 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1020

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
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Db       1021 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1050

RESULT 2
AAH16397
ID   AAH16397 standard; cDNA; 1574 BP.
XX
AC   AAH16397;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:15359.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
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```
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 15359; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 1574 BP; 420 A; 361 C; 372 G; 421 T; 0 other;

Alignment Scores:
Pred. No.:                4.62e-178       Length:          1574
Score:                    1799.00         Matches:         350
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       22              Gaps:            0

US-09-745-506-37 (1-350) x AAH16397 (1-1574)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
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Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
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Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
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Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
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Db        451 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 510

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 570

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 630

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
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Db        631 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 690

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
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Db        691 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 750

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 810

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 870

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 930

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 990

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1050

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1110

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
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Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
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Db       1231 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1290

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
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Db       1291 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1320

RESULT 3
AAK60866
ID   AAK60866 standard; cDNA; 1696 BP.
XX
AC   AAK60866;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:5926.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01354.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
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PR 08-NOV-2000; 2000US-0246475.
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PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
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PR 08-DEC-2000; 2000US-0251868.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR P-PSDB; AAM88085.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Claim 1; SEQ ID NO 5926; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased

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CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic-related diseases, especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 1696 BP; 510 A; 369 C; 379 G; 435 T; 3 other;

Alignment Scores:
Pred. No.:              5.15e-178      Length:          1696
Score:                  1799.00        Matches:         350
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     22             Gaps:            0

US-09-745-506-37 (1-350) x AAK60866 (1-1696)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 366

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 426

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 486

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 546

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 606

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 666

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 726

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 786

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 846

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 906

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 966

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 1026

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1086

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1146

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1206

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1266

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1326

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              ||||||||||||||||||||||||||||||
Db       1327 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1356

RESULT 4
ABV23243
ID   ABV23243 standard; cDNA; 1739 BP.
XX
AC   ABV23243;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 23234.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 4189-4190; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
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CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 1739 BP; 457 A; 389 C; 411 G; 473 T; 9 other;

Alignment Scores:
Pred. No.:              5.34e-178       Length:         1739
Score:                  1799.00         Matches:        350
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     23              Gaps:           0

US-09-745-506-37 (1-350) x ABV23243 (1-1739)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 356

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 416

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 476

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 536

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 596

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 656

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 716

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 776

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 836

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 896

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 956

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 1016

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1076

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1136

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1196

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1256

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1316

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              ||||||||||||||||||||||||||||||
Db       1317 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1346
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RESULT 5
ABV29087
ID   ABV29087 standard; cDNA; 1739 BP.
XX
AC   ABV29087;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 29078.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 6170; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
```

```
SQ   Sequence 1739 BP; 457 A; 389 C; 411 G; 473 T; 9 other;

Alignment Scores:
Pred. No.:              5.34e-178       Length:         1739
Score:                  1799.00         Matches:        350
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     23              Gaps:           0

US-09-745-506-37 (1-350) x ABV29087 (1-1739)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 356

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 416

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 476

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 536

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 596

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 656

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 716

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 776

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 836

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 896

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 956

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 1016

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1076

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1136

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1196

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1256

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1316

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              |||||||||||||||||||||||||||||
Db       1317 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1346
```

```
RESULT 6
AAS44644
ID   AAS44644 standard; DNA; 1554 BP.
XX
AC   AAS44644;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human full-length polynucleotide sequence #69.
XX
KW   Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW   mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW   cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW   nervous system disorder; inflammatory disorder; cell differentiation; ds;
KW   angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW   genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW   cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory;
KW   antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW   neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
KW   immunostimulant; analgesic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200164834-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04926.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
PR   17-JUN-2000; 2000US-0597707.
PR   14-JUL-2000; 2000US-0616807.
PR   19-SEP-2000; 2000US-0664641.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Asundi V,  Zhang J,  Zhao QA,  Ren F;
PI   Xue AJ,  Yang Y,  Wehrman T,  Wang J,  Ma Y,  Wang D,  Chen R,  Xu C;
PI   Drmanac R;
XX
DR   WPI; 2001-589862/66.
DR   P-PSDB; AAU27744.
XX
PT   Novel polypeptides and nucleic acids obtained from cDNA libraries
PT   prepared from various human tissues, for diagnosis, treatment of
PT   cancer, neurological, inflammatory disorders and for use in arrays for
PT   detection -
XX
PS   Claim 1; SEQ ID No 69; 153pp; English.
XX
CC   Sequences AAS44576-AAS44919 represent full-length polynucleotides and
CC   contig polynucleotides encoding polypeptides of the invention. The DNA
CC   and protein sequences are useful for the treatment, diagnosis and
CC   prevention of various types of disorder in a mammalian subject such as a
CC   human, dog, monkey, mouse, hamster or rat. The disorders include cancers
CC   such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
CC   as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC   diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC   disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC   chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC   Wernicke disease, inflammatory disorders such as nephritis, Crohn's
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CC   disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
CC   bowel disease. The sequences exhibit activity relating to angiogenesis,
CC   cell proliferation, cell differentiation, stem cell growth factor,
CC   activin or inhibin. Therefore, they can be used to manipulate stem cells
CC   in culture to give rise to neuroepithelial cells that can be used to
CC   augment or replace cells damaged by illness, accidental damage or genetic
CC   disorders. The sequences may also be used for regeneration of bone,
CC   cartilage, tendons and ligaments and in tissue repair and burn healing.
CC   Note: Some sequences for this patent did not form part of the printed
CC   specification, but were obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1554 BP; 428 A; 358 C; 346 G; 422 T;. 0 other;

Alignment Scores:
Pred. No.:                1.92e-177       Length:          1554
Score:                    1793.00         Matches:         349
Percent Similarity:       99.71%          Conservative:    0
Best Local Similarity:    99.71%          Mismatches:      1
Query Match:              99.67%          Indels:          0
DB:                       22              Gaps:            0

US-09-745-506-37 (1-350) x AAS44644 (1-1554)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 295

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 355

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 415

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 475

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 535

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 595

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 655

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 715

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 775

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 835

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 895

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 955

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1015

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1075

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       1076 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATATTTTGGATGCT 1135

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1195

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1255

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
              |||||||||||||||||||||||||||||
Db       1256 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1285

RESULT 7
AAF59945
ID   AAF59945 standard; cDNA; 1398 BP.
XX
AC   AAF59945;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human gene expression regulatory factor-related protein hNIF3-s cDNA.
XX
KW   Human gene expression regulatory factor-related protein; hNIF3-s;
KW   NGG1-interacting factor; haemopoietic stem cell; preparation;
KW   detection; ss.
XX
OS   Homo sapiens.
XX
PN   CN1272543-A.
XX
PD   08-NOV-2000.
XX
PF   11-APR-2000; 2000CN-0115369.
XX
PR   11-APR-2000; 2000CN-0115369.
XX
PA   (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
XX
PI   Li N,  Xiao H,  Liu F;
XX
DR   WPI; 2001-183596/19.
DR   P-PSDB; AAB60663.
XX
PT   Human gene expression regulatory factor related protein and its coded
PT   sequence -
XX
PS   Claim 1; Page 18-19; 20pp; Chinese.
XX
CC   The invention relates to a novel human gene expression regulatory
CC   factor-related protein, hNIF3-s (NGG1-interacting factor, AAB60663),
CC   and cDNA encoding it (AAF59945). hNIF3-s is expressed in haemopoietic
CC   stem cells. The invention also relates to the preparation of hNIF3-s
CC   proteins and nucleic acids, and the detection of hNIF3-s proteins and
CC   nucleic acids in a sample. The present sequence represents cDNA encoding
CC   hNIF3-s.
XX
SQ   Sequence 1398 BP; 365 A; 331 C; 342 G; 360 T; 0 other;

Alignment Scores:
Pred. No.:                2.26e-174       Length:          1398
Score:                    1763.00         Matches:         349
Percent Similarity:       99.15%          Conservative:    1
```

```
Best Local Similarity:  98.87%          Mismatches:     0
Query Match:            98.00%          Indels:         3
DB:                     22              Gaps:           0

US-09-745-506-37 (1-350) x AAF59945 (1-1398)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 295

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 355

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 415

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIle-ThrTrpAsnTh 80
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        416 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATTAACCTGGAACAC 475

Qy         80 rTrp--LysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerPro 99
              ||||  :::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 ATGGGAAGGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCT 535

Qy        100 HisThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CATACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGA 595

Qy        120 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsn 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GCTTGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAAC 655

Qy        140 HisArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaVal 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CACCGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTG 715

Qy        160 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGln 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 AAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAA 775

Qy        180 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSer 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 ACACGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCC 835

Qy        200 ArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeu 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 CGGAACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTA 895

Qy        220 HisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIle 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CATACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATT 955

Qy        240 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 GATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGA 1015

Qy        260 ThrLeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeu 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 ACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTG 1075

Qy        280 GlnGlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAsp 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 CAGGGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGAT 1135

Qy        300 AlaAlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPhe 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 GCTGCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTT 1195

Qy        320 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 CTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTA 1255

Qy        340 SerGluThrAspArgAspProLeuGlnValVal 350
              |||||||||||||||||||||||||||||||||
Db       1256 TCAGAGACTGACAGGGACCCTCTTCAGGTGGTA 1288

RESULT 8
ABL60919
ID   ABL60919 standard; cDNA; 1385 BP.
XX
AC   ABL60919;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human protein kinase C 27.17 polypeptide encoding cDNA.
XX
KW   Human; protein kinase C 27.17; protein metabolism; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             389..1132
FT                   /*tag= a
FT                   /product= "protein kinase C 27.17 polypeptide"
XX
PN   CN1333355-A.
XX
PD   30-JAN-2002.
XX
PF   07-JUL-2000; 2000CN-0117049.
XX
PR   07-JUL-2000; 2000CN-0117049.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-305609/35.
DR   P-PSDB; ABB08182.
XX
PT   Human protein kinase C 27.17 polypeptide and its encoding
PT   polynucleotide, for treating e.g. protein metabolism disturbance -
XX
PS   Claim 6; Page 25-26 (disclosure); 33pp; Chinese.
XX
CC   The invention relates to a human protein kinase C 27.17 polypeptide and
CC   its encoding polynucleotide. The polypeptide can be expressed by standard
CC   DNA recombination. The polynucleotide, polypeptide and its antagonist are
CC   useful for treating e.g. protein metabolism disturbance. The present
CC   sequence represents the human protein kinase C 27.17 polypeptide encoding
CC   cDNA.
XX
SQ   Sequence 1385 BP; 375 A; 324 C; 308 G; 378 T; 0 other;

Alignment Scores:
Pred. No.:              1.87e-170       Length:         1385
Score:                  1725.50         Matches:        344
Percent Similarity:     98.57%          Conservative:   1
Best Local Similarity:  98.29%          Mismatches:     5
Query Match:            95.91%          Indels:         2
DB:                     24              Gaps:           0

US-09-745-506-37 (1-350) x ABL60919 (1-1385)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 141

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 201

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        202 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 261

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 321

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 381

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 441

Qy        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
             |||||||||||||||   ||||||||||   ||||||:::|||      |||   |||
Db        442 TGTACCTCCAGGCCATA-CATCCTTCCAAGCT-CCCAACTTCCCCTACAGAGGAACCCAC 499

Qy        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 559

Qy        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 619

Qy        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 679

Qy        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 739

Qy        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 799

Qy        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 859

Qy        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 919

Qy        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 979

Qy        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1039

Qy        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1040 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1099

Qy        341 GluThrAspArgAspProLeuGlnValVal 350
             ||||||||||||||||||||||||||||||
Db       1100 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1129

RESULT 9
AAS85172/c
ID   AAS85172 standard; cDNA; 1686 BP.
XX
AC   AAS85172;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #20976.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG20985.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 20976; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1686 BP; 445 A; 397 C; 391 G; 452 T; 1 other;

Alignment Scores:
Pred. No.:              2.36e-116      Length:          1686
Score:                  1209.50        Matches:         308
Percent Similarity:     83.55%         Conservative:    7
Best Local Similarity:  81.70%         Mismatches:      32
Query Match:            67.23%         Indels:          30
DB:                     23             Gaps:            10

US-09-745-506-37 (1-350) x AAS85172 (1-1686)

Qy          1 MetAspLeuLys-AlaLeuLeuSerSerLeu-AsnAspPheAla---SerLeuSerPheA 19
              |||||||||||| |||||||||||||||||| |||||||||         |||   ||||
Db       1383 ATGGATTTGAAGAGCTCTCCTTTCTTCCTTGGAATGACTTTTGCATCCCTCTTCGTTTTG 1324

Qy         19 laGluSerTrpAspAsn---ValGlyLeuLeuVal-GluPro-SerProProHis-ThrV 37
              ||||||||||          :::|||||||||||| ||||||    |||||||||    |
Db       1323 CTGAGAGTTGGGGACAATGTTTGGGATTACTGGTGGGAACCAAGGCCCACCACATAANTG 1264

Qy         37 alAsn---ThrLeuPheLeuThrAsnAspLeuThrGlu---GluValMetGluGluValL 55
              ||      ||||||      ||||||||||||||||||         |||||||
Db       1263 TTAAATACACTCTTTCCTGGACCAATGACCTGACTGAGGGAAGTGATGGGAGGGAGGTGC 1204
```

```
Qy         55 euGlnLysLys-AlaAspLeuIleLeuSerTyr-HisProPro-IlePhe-ArgProMet 73
Db       1203 TGCAAAAGAAGGGCAGACCTCATTCTCTCCTACCCATCCGCCTTATCTTCCCGACCCATG 1144

Qy         74 Lys---ArgIleThrTrpAsnThrTrp-LysGluArgLeuValIleArgAlaLeuGluAs 92
Db       1143 GAAGGCGCATTAACCGGGAACACATGGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAA 1084

Qy         92 nArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyValAsnAs 112
Db       1083 CAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAA 1024

Qy        112 nTrpLeuAlaLysGlyLeuGlyAlaCysThrSerArgProIleHisProSerLysAlaPr 132
Db       1023 CTGGTTGGCTAAAGGGCTTGGAGCTTGTACCTCCAGGCCCATACATCCTTCCAAAGCTCC 964

Qy        132 oAsnTyrProThrGluGlyAsnHisArgValGluPheAsnValAsnTyrThrGlnAspLe 152
Db        963 CAACTACCCTACAGAGGGAAACCACCGAGTAGAATTCAACGTTAACTACACCCAAGACCT 904

Qy        152 u-AspLysValMetSer-AlaValLysGlyIle-AspGlyValSerValThrSerPheSe 171
Db        903 GGGACAAAGTCATGTCTGGCAGTGAAAGGAATTTGACGGTGTTTCTGTCACTTCTTTTTC 844

Qy        171 rAlaArgThrGlyAsnGluGluGlnThrArgIleAsnLeuAsnCysThrGlnLysAlaLe 191
Db        843 TGCTAGGACTGGTAATGAGGAACAAACACGGATTAATCTGAATTGTACTCAGAAGGCTTT 784

Qy        191 uMetGlnValValAspPheLeuSerArgAsnLysGlnLeuTyrGlnLysThrGluIleLe 211
Db        783 GATGCAGGTGGTAGATTTTCTTTCCCGGAACAAACAACTTTATCAGAAGACGGAAATTCT 724

Qy        211 uSerLeuGluLysProLeuLeuLeuHisThrGlyMetGlyArgLeuCysThrLeuAspGl 231
Db        723 GTCACTGGAGAAGCCTTTGCTTCTACATACTGGAATGGGACGGTTATGCACACTGGATGA 664

Qy        231 uSerValSerLeuAlaThrMetIleAspArgIleLysArgHisLeuLysLeuSerHisIl 251
Db        663 ATCTGTCTCCCTGGCAACCATGATTGATCGAATAAAAAGACACCTAAAACTATCTCATAT 604

Qy        251 eArgLeuAlaLeuGlyValGlyArgThrLeuGluSerGlnValLysValValAlaLeuCy 271
Db        603 TCGCTTAGCCCTTGGGGTGGGGAGAACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTG 544

Qy        271 sAlaGlySer-GlySerSerValLeuGlnGlyValGluAlaAspLeuTyrLeuThr---- 289
Db        543 TGCTGGTTCTGGGGAGCAGCGTTCTGCAGGGTGTTGAGGGCTGACCCTTTACCTCACAGG 484

Qy        290 --GlyGluMetSerHisHisAspThrLeu-AspAlaAlaSer-GlnGlyIle-AsnVal- 307
Db        483 TAGGTGAGATGTCCCATCATGATATTTTGGGATGCTGCTTCCCCAAGGAATTAAATGTCA 424

Qy        308 IleLeuCysGlu---HisSerAsnThrGluArgGlyPhe---LeuSerAsp-LeuArgAs 325
Db        423 ATCCTCTGTGAAACACCAGCAAACACTGAACGAGGCCTTTCCTTTCCTGACCCTCCGAGA 364

Qy        325 pMetLeuAsp---SerHisLeuGluAsnLysIleAsnIleIle---LeuSerGluThrAs 343
Db        363 TATGCCTGGAATCCTCACCTTGGAGAATAAGATAAATATTATCCCTATCCAGAGACCTGA 304

Qy        343 pArgAspProLeu 347
Db        303 CAGGGACCCTCTT 291
```

```
RESULT 10
AAH07192
ID   AAH07192 standard; cDNA; 796 BP.
XX
AC   AAH07192;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:4027.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 1; SEQ ID 4027; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 796 BP; 192 A; 204 C; 202 G; 195 T; 3 other;
```

```
Alignment Scores:
Pred. No.:              9.09e-77        Length:         796
Score:                  826.50          Matches:        170
Percent Similarity:     96.59%          Conservative:   0
Best Local Similarity:  96.59%          Mismatches:     6
Query Match:            45.94%          Indels:         3
DB:                     22              Gaps:           0

US-09-745-506-37 (1-350) x AAH07192 (1-796)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
Db        271 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 330

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
Db        331 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 390
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Qy        41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       391 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 450

Qy        61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       451 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 510

Qy        81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       511 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 570

Qy       101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       571 ACAGCCTATGATGCTGCGCCCCAAGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 630

Qy       121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
             ||||||  ||||||||||||||||||||||||  ||||||||||||||||||||
Db       631 TGTACCTTCAGGCCCATACATCCTTCCAAAGCTCCAAC-TACCCTACAGAGGGAAACCAC 689

Qy       141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
             |||  ||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       690 CGATA-GAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCANTGAAA 748

Qy       161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsn 176
             ||||||||||||||||||||      ||||||||||||||||||||
Db       749 GGAATTGACGGNGTTTCTGTCCTTC--TTTTCTGCTAGGACTGGTAAT 794
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RESULT 11
AAK78763
ID AAK78763 standard; DNA; 14969 BP.
XX
AC AAK78763;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33575.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.

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PR   08-NOV-2000; 2000US-0246526.
PR   08-NOV-2000; 2000US-0246527.
PR   08-NOV-2000; 2000US-0246528.
PR   08-NOV-2000; 2000US-0246532.
PR   08-NOV-2000; 2000US-0246609.
PR   08-NOV-2000; 2000US-0246610.
PR   08-NOV-2000; 2000US-0246611.
PR   08-NOV-2000; 2000US-0246613.
PR   17-NOV-2000; 2000US-0249207.
PR   17-NOV-2000; 2000US-0249208.
PR   17-NOV-2000; 2000US-0249209.
PR   17-NOV-2000; 2000US-0249210.
PR   17-NOV-2000; 2000US-0249211.
PR   17-NOV-2000; 2000US-0249212.
PR   17-NOV-2000; 2000US-0249213.
PR   17-NOV-2000; 2000US-0249214.
PR   17-NOV-2000; 2000US-0249215.
PR   17-NOV-2000; 2000US-0249216.
PR   17-NOV-2000; 2000US-0249217.
PR   17-NOV-2000; 2000US-0249218.
PR   17-NOV-2000; 2000US-0249244.
PR   17-NOV-2000; 2000US-0249245.
PR   17-NOV-2000; 2000US-0249264.
PR   17-NOV-2000; 2000US-0249265.
PR   17-NOV-2000; 2000US-0249297.
PR   17-NOV-2000; 2000US-0249299.
PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-483426/52.
XX
PT   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and
PT   metastasis -
XX
PS   Disclosure; SEQ ID NO 33575; 3071pp + Sequence Listing; English.
XX
CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic-related diseases. especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 14969 BP; 4016 A; 3069 C; 3042 G; 4842 T; 0 other;
```

```
Alignment Scores:
Pred. No.:              1.55e-65        Length:         14969
Score:                  737.00          Matches:        172
Percent Similarity:     37.23%          Conservative:   0
Best Local Similarity:  37.23%          Mismatches:     1
Query Match:            40.97%          Indels:         290
DB:                     22              Gaps:           1

US-09-745-506-37 (1-350) x AAK78763 (1-14969)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2604 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 2663

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2664 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 2723

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2724 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 2783

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2784 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 2843

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2844 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 2903

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeu------ 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2904 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCT-TGGTGA 2962

Qy        118 ------------------------------------------------------------ 118

Db       2963 GAAGCCTCTTTCATATTTGATATTTTCCCTGCAAATACTTTGAAACTTTAGGATGTCTTT 3022

Qy        118 ------------------------------------------------------------ 118

Db       3023 CCAGTAAAGTTTTAACTGCTTTAGGGTTGGGGAGGGCATGATTCCATTTTTATATAATAA 3082

Qy        118 ------------------------------------------------------------ 118

Db       3083 TTTTAAAATAATGTTGCTGAAATTTGGCAGTTAAATTGCATTTGAAAAAGGAAACATTTT 3142

Qy        118 ------------------------------------------------------------ 118

Db       3143 TTATTCTTATGGAGTAAGGAGAGCAGAAGTCTTCCTTACTGGACTGAGCTTCATGATTCC 3202

Qy        118 ------------------------------------------------------------ 118

Db       3203 TCACTTTTGTGGCACAATGCCTGTCACCCAGGCACTTGGAAAATGCTTGTTGAATTGAAA 3262

Qy        118 ------------------------------------------------------------ 118

Db       3263 GCTCAGGCCTCTCCAGAATACACTTGATTGATAAGTCAAGTAAATAGACATCAGGGTTTT 3322

Qy        118 ------------------------------------------------------------ 118

Db       3323 AATGAATGTTTTTAGTGAATGTTTACTTATGCCTAGCACAATGAGGGAATGATGGATGGA 3382

Qy        118 ------------------------------------------------------------ 118

Db       3383 TTTTAGCTTTATTTTAGTAAGTCTTTAGTTTACTCATTTTGGGCTAAAGCTTTTATGATG 3442

Qy        118 ------------------------------------------------------------ 118

Db       3443 ATATCTGGATTAATGTGGTCAAATAAAGTATGAGCATTTGCAACCTGAATGATGGTTTAC 3502

Qy        118 ------------------------------------------------------------ 118

Db       3503 ATGGCTAGATTTACCAAGCAGTAGACCATTCTGTGTATTATCTGAAAATGTATGAATCAG 3562
```

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Qy        118 ------------------------------------------------------------ 118

Db       3563 TCTTTCTTGTCCAAGTTTTTCAGAGATTTAAGAATCTTTTGGAAAATAATTCTGAAAATA 3622

Qy        118 ------------------------------------------------------------ 118

Db       3623 ATTTGATTTTGTATGTCCATGCCAAAGCCCTAGATTATGGGGACTGGTGATGTATATCTA 3682

Qy        118 ------------------------------------------------------------ 118

Db       3683 AGGGATGTGTGTATGTTATGTAAGCATGAGAATGAATCTTTTTAAAAAGTCATTTCTTAG 3742

Qy        118 ------------------------------------------------------------ 118

Db       3743 AAATTTTGCCTATAATAGTTTACTTTTAAATCTTAATCTCTCACCCCCCAAAACTCCCAT 3802

Qy        119 --------------------GlyAlaCysThrSerArgProIleHisProSerLysAla 131
                                 |||||||||||||||||||||||||||||||||||||
Db       3803 TTTCCCACAATATTTTCTCTAGGAGCTTGTACCTCCAGGCCCATACATCCTTCCAAAGCT 3862

Qy        132 ProAsnTyrProThrGluGlyAsnHisArgValGluPheAsnValAsnTyrThrGlnAsp 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3863 CCCAACTACCCTACAGAGGGAAACCACCGAGTAGAATTCAACGTTAACTACACCCAAGAC 3922

Qy        152 LeuAspLysValMetSerAlaValLysGlyIleAspGlyValSerValThrSerPheSer 171
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3923 CTGGACAAAGTCATGTCTGCAGTGAAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCT 3982

Qy        172 AlaArg 173
               ||||||
Db       3983 GCTAGG 3988
```

RESULT 12
AAL23953
ID AAL23953 standard; cDNA; 462 BP.
XX
AC AAL23953;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 16410.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1; Page 3004; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 462 BP; 103 A; 126 C; 118 G; 115 T; 0 other;

Alignment Scores:

Pred. No.:	5.04e-58	Length:	462
Score:	644.00	Matches:	122
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	35.80%	Indels:	0
DB:	22	Gaps:	0

US-09-745-506-37 (1-350) x AAL23953 (1-462)

```
Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 155

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 215

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 275

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 335

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 395

Qy        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 455

Qy        121 CysThr 122
              ||||||
Db        456 TGTACC 461
```

RESULT 13
AAL15105
ID AAL15105 standard; cDNA; 514 BP.
XX
AC AAL15105;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 7562.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.

```
PR   09-JUN-2000; 2000US-0211315.
PR   25-JUL-2000; 2000US-0220534.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS   Claim 1; Page 1361; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity.
XX
SQ   Sequence 514 BP; 113 A; 141 C; 130 G; 126 T; 4 other;

Alignment Scores:
Pred. No.:                1.46e-53      Length:          514
Score:                    602.00        Matches:         119
Percent Similarity:       96.77%        Conservative:    1
Best Local Similarity:    95.97%        Mismatches:      2
Query Match:              33.46%        Indels:          2
DB:                       22            Gaps:            0

US-09-745-506-37 (1-350) x AAL15105 (1-514)

Qy          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 181

Qy         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 241

Qy         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 301

Qy         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 361

Qy         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsn-ArgValGlyIleTyrSerProHi 100
              |||||||||||||||||||||||||||||||    ||| :::|||||||||||||||||||
Db        362 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGANAACAAAAGTCGGTATCTACTCTCCTCA 421

Qy        100 sThrAlaTyrAspAlaAlaProGlnGlyVal-AsnAsnTrpLeuAlaLysGlyLeuGlyA 120
              |||||||||||||||||||||||||||||| |||||||||||||||   ||||||
Db        422 TACAGCCTATGATGCTGCGCCCCAAGGCGTTCAACAACTGGTTGGCTAAANGGCTTGGAG 481

Qy        120 laCysThr 122
              ||||||||
Db        482 CTTGTACC 489

RESULT 14
ABL07427
ID   ABL07427 standard; cDNA; 1011 BP.
XX
AC   ABL07427;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 16763.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB63324.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 16763; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1011 BP; 291 A; 230 C; 243 G; 247 T; 0 other;

Alignment Scores:
Pred. No.:                1.27e-50      Length:          1011
Score:                    578.00        Matches:         118
Percent Similarity:       51.44%        Conservative:    61
Best Local Similarity:    33.91%        Mismatches:      81
Query Match:              32.13%        Indels:          88
DB:                       23            Gaps:            4

US-09-745-506-37 (1-350) x ABL07427 (1-1011)

Qy          3 LeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGluSerTrp 22
              |||   |||::::::      |||   :::|||||||      |||:::||||||   |||
Db         80 CTGGCGGCTGTGGTCAAGGAGCTGGAGAACTTTGCTCCGACTTCTTGGGCAGAGAAGTGG 139

Qy         23 AspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeuPheLeu 42
              ||||||||||||||||:::||||||                 :::      :::   |||
Db        140 GACAATGTGGGACTCCTGATCGAACCGCACCGCGAAAAACAAATCAAGAAAATACTATTA 199

Qy         43 ThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAspLeuIle 62
              ||||||||||||||||   |||::::::|||   |||:::|||:::|||:::||||||
Db        200 ACTAACGATTTAACCGAGCCCGTAGTGAAAGAAGCGCTAGAGAAGGAGGCGGAGCTCATA 259

Qy         63 LeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThrTrpLys 82
              :::|||||||||||||||||:::|||:::   |||||||||   :::   ||||||
Db        260 ATCAGCTATCATCCGCCAATTTTCAAGCCCCTGACCAGGATTACGCAGTCACATTGGAAG 319

Qy         83 GluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHisThrAla 102
              ||||||:::|||          |||   |||   :::   :::|||||||||||||||||
Db        320 GAGCGCGTGGTGGCAGCATGCTTGGCCAACGATATAGCCTTGTACTCGCCCCACACGGCG 379

Qy        103 TyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAlaCysThr 122
              :::|||            |||||||||:::|||||||:::|||   :::         :::
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```
Db        380 TGGGATAAGAAGAGTGGTGGCGTCAACGACTGGCTATCTAAGGCAGTGAATATCATCAGC 439

Qy        123 SerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArgVal 142
                  ||||||:::   |||
Db        440 ATCCGCCCTCTGGAACCGGAG---------------------------------------- 460

Qy        143 GluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIle 162
                                                 :::   |||      |||
Db        461 ---------------------------------------TTGGGTGCTCCTCCGGGT--- 478

Qy        163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIle 182

Db        478 ------------------------------------------------------------ 478

Qy        183 AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLys 202

Db        478 ------------------------------------------------------------ 478

Qy        203 GlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHisThrGly 222
                                                                    ||||||
Db        479 ----------------------------------------------------ACCGGA 484

Qy        223 MetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIle 242
                  ||||||         ::::::      :::   |||:::   :::::::::   :::
Db        485 TCCGGTAGATAT------ATAGAAACCAAAATGGAGCTTTCCCAGGTGGTGGAGTCTCTG 538

Qy        243 LysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGlu 262
                  ::::::   ::::::   |||   :::   :::||||||   ||||||   |||   :::
Db        539 CAAAAGCGCATTAGAAACAGC---GTGCACGTTGCTCTAGCTGTGGGCCACACCCCCAAG 595

Qy        263 SerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGlnGlyVal 282
                  :::   ::::::   |||   :::|||||||||||||||||:::|||:::|||:::|||:::
Db        596 ACACTCATCCAATCCGTCGGCATTTGTGCCGGCTCTGGAGCATCTCTGCTGAAGGGTATC 655

Qy        283 GluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAlaAlaSer 302
                  :::|||||||||   :::|||||||||||||||||||||:::   |||:::
Db        656 CAAGCGGATCTTATCATTACCGGCGAAATGTCCCATCACGAAGTTCTGGAGTTTACTCAC 715

Qy        303 GlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeuSerAsp 322
                        |||:::||||||   ||||||||||:::||||||||||||||||   :::
Db        716 AACAATACCACCGTTCTTCTCTGCAATCATAGTAATTCAGAAAGGGGTTTTCTCCATGAG 775

Qy        323 LeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSerGluThr 342
                        :::|||         |||       :::       :::   :::||||||
Db        776 TTTTGCCCTATATTGGCCAAATCTTTAAATGAAGAATGCCTGGTATTTGTATCTGAAGTG 835

Qy        343 AspArgAspProLeuGlnValVal 350
                  |||:::||||||||||      |||
Db        836 GACAAGGATCCTCTGGTCACCGTG 859

RESULT 15
ABL10022
ID   ABL10022 standard; cDNA; 2967 BP.
XX
AC   ABL10022;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 24548.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB65919.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 24548; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2967 BP; 844 A; 651 C; 669 G; 803 T; 0 other;

Alignment Scores:
Pred. No.:              6.18e-50      Length:          2967
Score:                  578.00        Matches:         118
Percent Similarity:     51.44%        Conservative:    61
Best Local Similarity:  33.91%        Mismatches:      81
Query Match:            32.13%        Indels:          88
DB:                     23            Gaps:            4

US-09-745-506-37 (1-350) x ABL10022 (1-2967)

Qy          3 LeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGluSerTrp 22
                |||   |||::::::      |||   :::||||||      |||:::|||||||   |||
Db         66 CTGGCGGCTGTGGTCAAGGAGCTGGAGAACTTTGCTCCGACTTCTTGGGCAGAGAAGTGG 125

Qy         23 AspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeuPheLeu 42
                |||||||||||||||||||:::||||||                :::     :::   |||
Db        126 GACAATGTGGGACTCCTGATCGAACCGCACCGCGAAAAACAAATCAAGAAAATACTATTA 185

Qy         43 ThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAspLeuIle 62
                |||||||||||||||||   |||::::::|||   |||:::|||:::|||:::||||||
Db        186 ACTAACGATTTAACCGAGCCCGTAGTGAAAGAAGCGCTAGAGAAGGAGGCGGAGCTCATA 245

Qy         63 LeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThrTrpLys 82
                :::|||||||||||||||||||||:::|||:::   |||||||||   :::   ||||||
Db        246 ATCAGCTATCATCCGCCAATTTTCAAGCCCCTGACCAGGATTACGCAGTCACATTGGAAG 305

Qy         83 GluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHisThrAla 102
                ||||||:::|||         |||   |||   :::   :::||||||||||||||||||
Db        306 GAGCGCGTGGTGGCAGCATGCTTGGCCAACGATATAGCCTTGTACTCGCCCCACACGGCG 365

Qy        103 TyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAlaCysThr 122
                :::|||           |||||||||:::|||||||:::|||   :::         :::
Db        366 TGGGATAAGAAGAGTGGTGGCGTCAACGACTGGCTATCTAAGGCAGTGAATATCATCAGC 425

Qy        123 SerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArgVal 142
                  ||||||:::   |||
Db        426 ATCCGCCCTCTGGAACCGGAG---------------------------------------- 446

Qy        143 GluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIle 162
                                                 :::   |||      |||
Db        447 ---------------------------------------TTGGGTGCTCCTCCGGGT--- 464

Qy        163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIle 182

Db        464 ------------------------------------------------------------ 464
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Qy        183 AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLys 202

Db        464 ------------------------------------------------------------ 464

Qy        203 GlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHisThrGly 222
                                                                      ||||||
Db        465 ------------------------------------------------------ACCGGA 470

Qy        223 MetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIle 242
                  ||||||         ::::::      :::   |||:::   :::::::::   :::
Db        471 TCCGGTAGATAT------ATAGAAACCAAAATGGAGCTTTCCCAGGTGGTGGAGTCTCTG 524

Qy        243 LysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGlu 262
              ::::::   ::::::   |||   :::   :::||||||   ||||||   |||   :::
Db        525 CAAAAGCGCATTAGAAACAGC---GTGCACGTTGCTCTAGCTGTGGGCCACACCCCCAAG 581

Qy        263 SerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGlnGlyVal 282
              :::   ::::::   |||   :::||||||||||||||||:::|||:::|||:::|||:::
Db        582 ACACTCATCCAATCCGTCGGCATTTGTGCCGGCTCTGGAGCATCTCTGCTGAAGGGTATC 641

Qy        283 GluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAlaAlaSer 302
              :::||||||||||   :::||||||||||||||||||||||:::   |||:::
Db        642 CAAGCGGATCTTATCATTACCGGCGAAATGTCCCATCACGAAGTTCTGGAGTTTACTCAC 701

Qy        303 GlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeuSerAsp 322
                      |||:::||||||   |||||||||:::|||||||||||||||   :::
Db        702 AACAATACCACCGTTCTTCTCTGCAATCATAGTAATTCAGAAAGGGGTTTTCTCCATGAG 761

Qy        323 LeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSerGluThr 342
                    :::|||          |||       :::       :::   :::||||||
Db        762 TTTTGCCCTATATTGGCCAAATCTTTAAATGAAGAATGCCTGGTATTTGTATCTGAAGTG 821

Qy        343 AspArgAspProLeuGlnValVal 350
              |||:::||||||||||      |||
Db        822 GACAAGGATCCTCTGGTCACCGTG 845
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Search completed: August 23, 2003, 18:33:24
Job time : 274 secs